

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 16:38:57 ; Search time 1672 Seconds  
(without alignments)  
434.706 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY\_NUC

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 1437254

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	15	100.0	17	6	AX352371 Sequence
3	15	100.0	22	6	AX352373 Sequence
4	15	100.0	25	6	I22533 Sequence 21
5	15	100.0	25	6	I47358 Sequence 21
6	14.6	97.3	25	6	I14212 Sequence 9
7	14.6	97.3	25	6	I22540 Sequence 28
8	14.6	97.3	25	6	I47365 Sequence 28
9	13.4	89.3	25	6	I22538 Sequence 26
10	13.4	89.3	25	6	I22783 Sequence 27
11	13.4	89.3	25	6	I47363 Sequence 26
12	13.4	89.3	25	6	I47608 Sequence 27
13	13	86.7	21	6	I12777 Sequence 75
14	13	86.7	22	6	I12778 Sequence 76
15	12.4	82.7	14	6	AX352367 Sequence
16	12.4	82.7	20	6	AX063311 Sequence
17	12.4	82.7	25	6	AR095910 Sequence
18	12.4	82.7	25	6	I22618 Sequence 10
19	12.4	82.7	25	6	I47443 Sequence 10

c	20	12.4	82.7	27	6	AR095909 Sequence
	21	11.8	78.7	15	6	AX352372 Sequence
	22	11.8	78.7	25	6	I22534 Sequence 22
	23	11.8	78.7	25	6	I47359 Sequence 22
c	24	11.4	76.0	18	6	BD089434 A method
	25	11.4	76.0	24	6	AR349788 Sequence
	26	11.4	76.0	30	6	A21743 oligonucleo
	27	11	73.3	20	6	BD177288 Sulfotran
	28	11	73.3	20	6	AX615193 Sequence
	29	11	73.3	20	6	AX643840 Sequence
	30	11	73.3	21	6	AX119403 Sequence
	31	11	73.3	29	6	BD182768 Novel (R)
	32	11	73.3	29	6	AX616507 Sequence
	33	10.8	72.0	14	6	AX352366 Sequence
c	34	10.8	72.0	18	6	BD093685 Human lp3
c	35	10.8	72.0	20	6	AR316227 Sequence
c	36	10.8	72.0	20	6	AR409583 Sequence
	37	10.8	72.0	20	6	AX231599 Sequence
	38	10.8	72.0	20	6	AX231709 Sequence
	39	10.8	72.0	23	6	BD143029 Method of
c	40	10.8	72.0	24	6	E24994 Apoptosis-1
c	41	10.8	72.0	24	6	AR397558 Sequence
	42	10.8	72.0	24	6	AX443853 Sequence
c	43	10.8	72.0	25	6	AX375203 Sequence
	44	10.8	72.0	25	6	AX447831 Sequence
	45	10.8	72.0	26	6	AR091105 Sequence

#### ALIGNMENTS

RESULT 1	AX352370	AX352370	15 bp	DNA	linear	PAT 06-FEB-2002
LOCUS	AX352370	Sequence 6 from Patent WO0175174.				
DEFINITION	AX352370	AX352370.1 GI:18617644				
ACCESSION	AX352370					
VERSION	AX352370.1					
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Cohenford, M.A. and Lentricchia, B.					
TITLE	Detection and typing of human papillomavirus using pna probes					
JOURNAL	Patent: WO 0175174-A 6 11-OCT-2001;					
	CYTYC CORPORATION (US)					
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Db	1	AGATACCACACGCAG	15						
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LOCUS	AX352371	17 bp	DNA	linear	PAT 06-FEB-2002				
DEFINITION	Sequence 7 from Patent WO0175174.								
ACCESSION	AX352371								
VERSION	AX352371.1 GI:18617645								
KEYWORDS	synthetic construct								
SOURCE	synthetic construct								
ORGANISM	other sequences; artificial sequences.								

REFERENCE 1  
AUTHORS Cohenford, M.A. and Lentrichia, B.  
TITLE Detection and typing of human papillomavirus using pna probes  
JOURNAL Patent: WO 0175174-A 7 11-OCT-2001;  
CYTYC CORPORATION (US)  
FEATURES Location/Qualifiers  
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Db 2 AGATACCACACGCAG 16  
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RESULT 3  
AX352373  
LOCUS AX352373 22 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 9 from Patent WO0175174.  
ACCESSION AX352373  
VERSION AX352373.1 GI:18617647  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Cohenford, M.A. and Lentrichia, B.  
TITLE Detection and typing of human papillomavirus using pna probes  
JOURNAL Patent: WO 0175174-A 9 11-OCT-2001;  
CYTYC CORPORATION (US)  
FEATURES Location/Qualifiers  
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Db 7 AGATACCACACGCAG 21  
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I22533  
LOCUS I22533 25 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 21 from patent US 5527898.  
ACCESSION I22533  
VERSION I22533.1 GI:1602887  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Bauer, H.M., Gravitt, P.E., Greer, C.E., Manos, M. Michele.,  
Reinick, R.M. and Zhang, T.Y.  
TITLE Detection of human papillomavirus by the polymerase chain reaction  
JOURNAL Patent: US 5527898-A 21 18-JUN-1996;  
FEATURES Location/Qualifiers  
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ORIGIN

Query Match 97.3%; Score 14.6; DB 6; Length 25;  
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Db 8 AGATACCACACGCAG 22  
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ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 25;  
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QY 1 AGATACCACACGCAG 15  
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Db 8 AGATACCACACGCAG 22  
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RESULT 5  
I47358  
LOCUS I47358 25 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 21 from patent US 5639871.  
ACCESSION I47358  
VERSION I47358.1 GI:2471323  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Bauer, H.M., Gravitt, P.E., Greer, C.E., Imprim, C.C.,  
Manos, M. Michele., Reinick, R.M. and Zhang, T.Y.  
TITLE Detection of human papillomavirus by the polymerase chain reaction  
JOURNAL Patent: US 5639871-A 21 17-JUN-1997;  
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Query Match 100.0%; Score 15; DB 6; Length 25;  
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Db 8 AGATACCACACGCAG 22  
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RESULT 6  
I14212  
LOCUS I14212 25 bp DNA linear PAT 26-SEP-1995  
DEFINITION Sequence 9 from patent US 5447839.  
ACCESSION I14212  
VERSION I14212.1 GI:997227  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 25)  
AUTHORS Manos, M. Michele., Bauer, H.M., Greer, C.E., Reinick, R.M. and Ting, Y.  
TITLE Detection of human papillomavirus by the polymerase chain reaction  
JOURNAL Patent: US 5447839-A 9 05-SEP-1995;  
FEATURES Location/Qualifiers  
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Query Match 97.3%; Score 14.6; DB 6; Length 25;  
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Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 8 AGATACCACACGCAG 22  
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RESULT 7  
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LOCUS I22540 25 bp DNA linear PAT 07-OCT-1996

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DEFINITION Sequence 28 from patent US 5527898.
ACCESSION I22540
VERSION I22540.1 GI:1602894
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
Resnick,R.M. and Zhang,T.Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5527898-A 28 18-JUN-1996;
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Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22

RESULT 8
LOCUS I47365 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 28 from patent US 5639871.
ACCESSION I47365
VERSION I47365.1 GI:2471330
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5639871-A 28 17-JUN-1997;
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Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22

RESULT 9
LOCUS I22538 25 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 26 from patent US 5527898.
ACCESSION I22538
VERSION I22538.1 GI:1602892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
Resnick,R.M. and Zhang,T.Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5527898-A 26 18-JUN-1996;
FEATURES
    Location/Qualifiers

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Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22

RESULT 10
LOCUS I22783 25 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 271 from patent US 5527898.
ACCESSION I22783
VERSION I22783.1 GI:1603137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
Resnick,R.M. and Zhang,T.Y.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5527898-A 271 18-JUN-1996;
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Qy 1 AGATACCACACGCAG 15
Db 8 AGATACCACACGCAG 22

RESULT 11
LOCUS I47363 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 26 from patent US 5639871.
ACCESSION I47363
VERSION I47363.1 GI:2471328
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5639871-A 26 17-JUN-1997;
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Db 8 AGATACCACACGCAG 22

RESULT 12
LOCUS I47363 25 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 26 from patent US 5639871.
ACCESSION I47363
VERSION I47363.1 GI:2471328
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Bauer,H.M., Gravitt,P.E., Greer,C.E., Imprim,C.C.,
Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
TITLE Detection of human papillomavirus by the polymerase chain reaction
JOURNAL Patent: US 5639871-A 26 17-JUN-1997;
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Db 8 AGATACCACACGCAG 22

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DEFINITION Sequence 271 from patent US 5639871.
ACCESSION  I47608
VERSION     I47608.1 GI:2471573
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Bauer, H.M., Gravitte, P.E., Greer, C.E., Imprim, C.C.,
            Manos, M.Michele, Resnick, R.M. and Zhang, T.Yi.
TITLE       Detection of human papillomavirus by the polymerase chain reaction
JOURNAL     Patent: US 5639871-A 271 17-JUN-1997;
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Query Match      89.3%; Score 13.4; DB 6; Length 25;
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACACGCGAG 15
Db      8 AGATACCACGCGAG 22
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RESULT 13
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DEFINITION Sequence 75 from patent US 5427930.
ACCESSION  I12777
VERSION     I12777.1 GI:910159
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Birkenmeyer, L.G., Carrino, J.J., Dille, B.J., Hu, H.-Y.,
            Kratochvil, J.D., Laffler, T.G., Marshall, R.L., Rinehardt, L.A. and
            Solomon, N.A.
TITLE       Amplification of target nucleic acids using gap filling ligase
JOURNAL     Patent: US 5427930-A 75 27-JUN-1995;
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LOCUS      I12778/c
DEFINITION Sequence 76 from patent US 5427930.
ACCESSION  I12778
VERSION     I12778.1 GI:910160
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
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REFERENCE   1 (bases 1 to 22)
AUTHORS     Birkenmeyer, L.G., Carrino, J.J., Dille, B.J., Hu, H.-Y.,
            Kratochvil, J.D., Laffler, T.G., Marshall, R.L., Rinehardt, L.A. and
            Solomon, N.A.
TITLE       Amplification of target nucleic acids using gap filling ligase
JOURNAL     Patent: US 5427930-A 76 27-JUN-1995;
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Db      13 GATACCACACGCA 1
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LOCUS      AX352367
DEFINITION Sequence 3 from Patent WO0175174.
ACCESSION  AX352367
VERSION     AX352367.1 GI:18617641
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    Cohenford, M.A. and Lentrichia, B.
REFERENCE   1
AUTHORS     Detection and typing of human papillomavirus using pna probes
TITLE       Patent: WO 0175174-A 3 11-OCT-2001;
JOURNAL     CVTVC CORPORATION (US)
FEATURES    Location/Qualifiers
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                        /note="PNA Probe III"
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Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Search completed: June 23, 2005, 18:52:40
Job time : 1675 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 16:28:51 ; Search time 418 Seconds  
(without alignments)  
212.431 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY NUC

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Total number of hits satisfying chosen parameters: 3522762

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Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	15	100.0	22	12	Ado08494 Human pap
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8	15	100.0	25	2	Aaq56337 Genital H
9	15	100.0	25	2	Aat44733 L1 consen
10	15	100.0	25	2	Aat77886 Human pap
11	15	100.0	25	2	Aavi7472 Primer FS
12	15	100.0	26	2	Aaq87034 Oligonucl
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14	14.6	97.3	25	2	Aat14761 L1 consen
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c 25	13	86.7	29	5	AAF61731	Aaf61731 E. coli C
c 26	13	86.7	29	5	AAF61734	Aaf61734 E. coli C
c 27	12.6	84.0	29	5	AAF61730	Aaf61730 E. coli C
28	12.4	82.7	14	5	AAI70564	Aai70564 Human pap
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31	12.4	82.7	20	4	AAF24619	Aaf24619 PCR prime
32	12.4	82.7	20	4	AAF24592	Aaf24592 PCR prime
33	12.4	82.7	25	2	AAQ56372	Aaq56372 L1 consen
34	12.4	82.7	25	2	AAT10812	Aat10812 Human pap
35	12.4	82.7	25	2	AAT44873	Aat44873 HPV L1 co
36	12.4	82.7	25	2	AAT77970	Aat77970 Human pap
37	12.4	82.7	25	9	ACI70339	Aci70339 Human mic
c 38	12.4	82.7	27	3	AZ235317	Aaz35317 Oligonucl
39	11.8	78.7	15	5	AAI70569	Aai70569 Human pap
40	11.8	78.7	15	12	ADO08493	Ado08493 Human pap
41	11.8	78.7	18	12	ADO16577	Ado16577 4 synthes
42	11.8	78.7	20	1	AAI90871	Aai90871 Promoter
43	11.8	78.7	20	12	ADH72332	Adh72332 Human for
44	11.8	78.7	20	13	ADR32107	Adr32107 Hepatitis
45	11.8	78.7	20	13	ADR67797	Adr67797 Hepatitis

#### ALIGNMENTS

#### RESULT 1

AAI70567  
ID AAI70567 standard; DNA; 15 BP.

XX AAI70567;

XX 21-JAN-2002 (first entry)

XX Human papillomavirus blocking probe VI.

XX HPV; probe; detection; typing; diagnosis; endocervical carcinoma;  
KW cervical cancer; neoplasia; probe; ss.

XX Human papillomavirus.

PN W0200175174-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010795.

XX 03-APR-2000; 2000US-0194304P.

XX 15-AUG-2000; 2000US-0225524P.

XX (CVTY-) CYTYC CORP.

XX Cohenford MA, Lentricchia B;

XX WPI; 2001-648563/74.

XX Detecting the presence of at least one selected strain of a disease  
organism or of a target nucleic acid of a human papilloma virus in a  
sample, comprises employing peptide-nucleic acid probes.

XX Claim 14; Page 24; 27pp; English.

XX The present sequence is that of nucleic acid probe VI, useful in the  
detection of human papillomavirus (HPV) nucleic acids. The probe is  
complementary to a portion of low-risk HPV strains 6 and 11, and binds to  
a portion between the binding sites for primer set MY09/MY11 (see  
AAI70571-72). The probe is used as a blocking probe to prevent  
amplification of nucleic acids from low-risk HPV strains while nucleic  
acids from high-risk strains to which the probe does not bind are

CC amplified by MY09/MY11. The method allows the specific detection of high-risk HPV nucleic acids and can be used to screen patient samples, e.g. cervical scrapings, for the presence of a high-risk HPV variant, especially type 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70. The presence of a particular target nucleic acid in sample cells is diagnostic of HPV infection, and may be indicative of risks of cancer, such as endocervical carcinoma, cervical cancer and neoplasia

XX Sequence 15 BP; 6 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15

Db 1 AGATACCACACGCAG 15

RESULT 2

ADO08491  
ID ADO08491 standard; DNA; 15 BP.

XX ADO08491;

DT 12-AUG-2004 (first entry)

XX Human papillomavirus (HPV) detection-related PNA probe VI SeqID23.

DE detection; typing; Human Papilloma Virus; HPV; infection; PNA probe;  
KW high-risk; infectious organism; probe; ss.

XX Human papillomavirus.

XX WO2004042071-A2.

XX 21-MAY-2004.

XX 07-OCT-2003; 2003WO-US031841.

XX 01-NOV-2002; 2002US-00286387.

XX (CYTY-) CYTYC CORP.

XX Cohenford MA, Lentricchia BB;

XX WPI; 2004-400683/37.

XX New peptide-nucleic acids, useful as a probe for detecting and typing Human Papilloma Virus infection, or in screening assay toward the diagnostically most-relevant strains or species of a disease organism.

XX Example 2; SEQ ID NO 23; 26pp; English.

XX This invention relates to a novel method for detection and typing of a Human Papilloma Virus (HPV) infection using PNA primers or probes, including methods for detecting high-risk types of HPV infection with minimal numbers of PNA probes or using PNA primers to selectively amplify only high-risk types of HPV. Specifically claimed are novel primer/probe sequences which are useful as primers/probes for detecting and typing HPV infection. The methods are used in a screening assay toward the diagnostically most-relevant strains or species of a disease organism or to selectively amplify high-risk strains of an infectious organism. The present sequence is that of a HPV PNA probe which was used in the exemplification of the invention.

XX Sequence 15 BP; 6 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15

Db 1 AGATACCACACGCAG 15

RESULT 3

AAI70568

ID AAI70568 standard; DNA; 17 BP.

XX AAI70568;

XX 21-JAN-2002 (first entry)

XX Human papillomavirus blocking probe VII.

XX HPV; probe; detection; typing; diagnosis; endocervical carcinoma;  
KW cervical cancer; neoplasia; probe; ss.

XX Human papillomavirus.

XX WO200175174-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010795.

XX 03-APR-2000; 2000US-0194304P.

XX 15-AUG-2000; 2000US-0225524P.

XX (CYTY-) CYTYC CORP.

XX Cohenford MA, Lentricchia B;

XX WPI; 2001-648563/74.

XX Detecting the presence of at least one selected strain of a disease organism or of a target nucleic acid of a human papilloma virus in a sample, comprises employing peptide-nucleic acid probes.

XX Claim 14; Page 25; 27pp; English.

XX The present sequence is that of nucleic acid probe VII, useful in the detection of human papillomavirus (HPV) nucleic acids. The probe is complementary to a portion of low-risk HPV strains 6 and 11, and binds to a portion between the binding sites for primer set MY09/MY11 (see AAI70571-72). The probe is used as a blocking probe to prevent amplification of nucleic acids from low-risk HPV strains while nucleic acids from high-risk strains to which the probe does not bind are amplified by MY09/MY11. The method allows the specific detection of high-risk HPV nucleic acids and can be used to screen patient samples, e.g. cervical scrapings, for the presence of a high-risk HPV variant, especially type 16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 68 and 70. The presence of a particular target nucleic acid in sample cells is diagnostic of HPV infection, and may be indicative of risks of cancer, such as endocervical carcinoma, cervical cancer and neoplasia

XX Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15

Db 2 AGATACCACACGCAG 16

RESULT 4

ADO08492  
ID ADO08492 standard; DNA; 17 BP.

XX ADO08492;

XX 12-AUG-2004 (first entry)

XX DE Human papillomavirus (HPV) detection-related PNA probe VII SeqID24.  
 XX KW detection; typing; Human Papilloma Virus; HPV; infection; PNA probe;  
 XX KW high-risk; infectious organism; probe; ss.  
 XX OS Human papillomavirus.  
 XX PN WO2004042071-A2.  
 XX PD 21-MAY-2004.  
 XX PF 07-OCT-2003; 2003WO-US031841.  
 XX PR 01-NOV-2002; 2002US-00286387.  
 XX PA (CVTY-) CYTYC CORP.  
 XX PI Cohenford MA, Lentricchia BB;  
 XX DR WPI; 2004-400683/37.  
 XX PT New peptide-nucleic acids, useful as a probe for detecting and typing  
 PT Human Papilloma Virus infection, or in screening assay toward the  
 PT diagnostically most-relevant strains or species of a disease organism.  
 XX PS Example 2; SEQ ID NO 24; 26pp; English.  
 XX SQ This invention relates to a novel method for detection and typing of a  
 CC Human Papilloma Virus (HPV) infection using PNA primers or probes,  
 CC including methods for detecting high-risk types of HPV infection with  
 CC minimal numbers of PNA probes or using PNA primers to selectively amplify  
 CC only high-risk types of HPV. Specifically claimed are novel primer/probe  
 CC sequences which are useful as primers/probes for detecting and typing HPV  
 CC infection. The methods are used in a screening assay toward the  
 CC diagnostically most-relevant strains or species of a disease organism or  
 CC to selectively amplify high-risk strains of an infectious organism. The  
 CC present sequence is that of a HPV PNA probe which was used in the  
 CC exemplification of the invention.  
 XX SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 15; DB 12; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGATACCACACGCAG 15  
 Db |||||  
 2 AGATACCACACGCAG 16  
 RESULT 5  
 AA170570  
 ID AA170570 standard; DNA; 22 BP.  
 XX AC AA170570;  
 XX DT 21-JAN-2002 (first entry)  
 XX DE Human papillomavirus modified consensus primer MC01.  
 XX KW HPV; probe; detection; typing; diagnosis; endocervical carcinoma;  
 KW cervical cancer; neoplasia; PCR primer; ss.  
 XX OS Human papillomavirus.  
 XX PN WO200175174-A2.  
 XX PD 11-OCT-2001.  
 XX PF 03-APR-2001; 2001WO-US010795.  
 XX PS 03-APR-2000; 2000US-0194304P.  
 PR

PR 15-AUG-2000; 2000US-0225524P.  
 XX (CVTY-) CYTYC CORP.  
 XX PI Cohenford MA, Lentricchia B;  
 XX DR WPI; 2001-648563/74.  
 XX PT Detecting the presence of at least one selected strain of a disease  
 PT organism or of a target nucleic acid of a human papilloma virus in a  
 PT sample, comprises employing peptide-nucleic acid probes.  
 XX PS Example 4; Page 25; 27pp; English.  
 XX SQ The present sequence is that of human papillomavirus (HPV) modified  
 CC consensus primer MC01. The primer was constructed for use with primer  
 CC MY09 (see AAI70571) and is capable of amplifying multiple HPV strains,  
 CC including strain 18. Use of probe VIII (see AAI70569) blocks  
 CC amplification of HPV strain 18 DNA. The invention provides methods for  
 CC the specific detection of high-risk type HPV nucleic acids. Patient  
 CC samples, e.g. cervical scrapings, can be screened for the presence of a  
 CC high-risk HPV variant, especially type 16, 18, 31, 33, 35, 39, 45, 51,  
 CC 52, 56, 58, 59, 68 and 70. The presence of a particular target nucleic  
 CC acid in sample cells is diagnostic of HPV infection, and may be  
 CC indicative of risks of cancer, such as endocervical carcinoma, cervical  
 CC cancer and neoplasia  
 XX SQ Sequence 22 BP; 8 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 15; DB 5; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGATACCACACGCAG 15  
 Db |||||  
 7 AGATACCACACGCAG 21  
 RESULT 6  
 ADO08494  
 ID ADO08494 standard; DNA; 22 BP.  
 XX AC ADO08494;  
 XX DT 12-AUG-2004 (first entry)  
 XX DE Human papillomavirus (HPV) detection-related PCR primer MC01 SeqID26.  
 XX KW detection; typing; Human Papilloma Virus; HPV; infection; PNA probe;  
 KW high-risk; infectious organism; MC01; PCR; primer; ss.  
 XX OS Human papillomavirus.  
 XX PN WO2004042071-A2.  
 XX PD 21-MAY-2004.  
 XX PF 07-OCT-2003; 2003WO-US031841.  
 XX PR 01-NOV-2002; 2002US-00286387.  
 XX PA (CVTY-) CYTYC CORP.  
 XX PI Cohenford MA, Lentricchia BB;  
 XX DR WPI; 2004-400683/37.  
 XX PT New peptide-nucleic acids, useful as a probe for detecting and typing  
 PT Human Papilloma Virus infection, or in screening assay toward the  
 PT diagnostically most-relevant strains or species of a disease organism.  
 XX PS Example 4; SEQ ID NO 26; 26pp; English.  
 PR

CC This invention relates to a novel method for detection and typing of a  
 CC Human Papilloma Virus (HPV) infection using PNA primers or probes,  
 CC including methods for detecting high-risk types of HPV infection with  
 CC minimal numbers of PNA probes or using PNA primers to selectively amplify  
 CC only high-risk types of HPV. Specifically claimed are novel primer/probe  
 CC sequences which are useful as primers/probes for detecting and typing HPV  
 CC infection. The methods are used in a screening assay toward the  
 CC diagnostically most-relevant strains or species of a disease organism or  
 CC to selectively amplify high-risk strains of an infectious organism. The  
 CC present sequence is that of a PCR primer, MC01, which was used in the  
 CC exemplification of the invention.  
 XX  
 SQ Sequence 22 BP; 8 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 12; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15  
 DB 7 AGATACCACACGCAG 21

RESULT 7  
 AAQ56371  
 ID AAQ56371 standard; DNA; 25 BP.

XX AC AAQ56371;

XX DT 25-MAR-2003 (revised)  
 XX DT 29-JUL-1994 (first entry)

XX DE L1 consensus probe FS10.

XX KW Human papilloma virus; amplification; polymerase chain reaction; PCR;  
 XX KW detection; assay; ss.

XX OS Synthetic.

XX PN US5283171-A.

XX PD 01-FEB-1994.

XX PF 15-FEB-1991; 91US-00651356.

XX PR 09-SEP-1988; 88US-00243486.

XX PR 10-MAR-1989; 89US-00322550.

XX PR 29-AUG-1989; 89WO-US003747.

XX PA (UYRP ) UNIV ROCHESTER.

XX PA (HOFF ) HOFFMANN LA ROCHE INC.

XX PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;

XX DR WPI; 1994-048082/06.

XX PT Detection of genital human papilloma virus - by PCR amplification using  
 XX PT defined consensus primer pairs.

XX PS Disclosure; Page 6; 13pp; English.

XX CC The sequence is that of Ls1 consensus probe FS10 which was used as part  
 XX CC of a simple and rapid assay method for detecting and typing HPV in  
 XX CC biological samples. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15  
 |||||

DB 8 AGATACCACACGCAG 22

RESULT 8  
 AAQ56337

ID AAQ56337 standard; DNA; 25 BP.

XX AC AAQ56337;

XX DT 25-MAR-2003 (revised)

XX DT 29-JUL-1994 (first entry)

XX DE Genital HPV L1 consensus positive strand primer FS10.

XX KW Human papilloma virus; amplification; polymerase chain reaction; PCR;  
 XX KW detection; assay; ss.

XX OS Synthetic.

XX PN US5283171-A.

XX PD 01-FEB-1994.

XX PF 15-FEB-1991; 91US-00651356.

XX PR 09-SEP-1988; 88US-00243486.

XX PR 10-MAR-1989; 89US-00322550.

XX PR 29-AUG-1989; 89WO-US003747.

XX PA (UYRP ) UNIV ROCHESTER.

XX PA (HOFF ) HOFFMANN LA ROCHE INC.

XX PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;

XX DR WPI; 1994-048082/06.

XX PT Detection of genital human papilloma virus - by PCR amplification using  
 XX PT defined consensus primer pairs.

XX PS Claim 5; Page 4; 13pp; English.

XX CC The sequence is that of the human papilloma virus (HPV) L1 consensus  
 XX CC positive strand primer FS10 which was used in the amplification by PCR of  
 XX CC HPV DNA. It may be used as part of a simple and rapid assay method for  
 XX CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003  
 XX CC to correct PF field.)

XX SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 15; DB 2; Length 25;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACACGCAG 15  
 |||||

DB 8 AGATACCACACGCAG 22

RESULT 9  
 AAT44733

ID AAT44733 standard; DNA; 25 BP.

XX AC AAT44733;

XX DT 25-MAR-2003 (revised)

XX DT 29-JAN-1997 (first entry)

XX DE L1 consensus positive strand primer FS10.

XX KW Probe; primer; PCR; polymerase chain reaction; amplification;  
 XX KW human papillomavirus; consensus; ss.

XX OS Synthetic.



XX PN US5527898-A.  
 XX PD 18-JUN-1996.  
 XX PF 07-JUN-1995; 95US-00474542.  
 XX PR 09-SEP-1988; 88US-00243486.  
 XX PR 10-MAR-1989; 89US-00322550.  
 XX PR 09-SEP-1989; 89WO-US003747.  
 XX PR 14-NOV-1990; 90US-00613142.  
 XX PR 20-APR-1993; 93US-00050743.  
 XX PR 24-SEP-1993; 93US-00126452.  
 XX PA (HOFF ) HOFFMANN LA ROCHE INC.  
 XX PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;  
 XX WPI; 1996-299903/30.  
 XX PT Nucleic acid hybridisation probes - specific for selected human papilloma  
 XX virus types.  
 XX PS Disclosure; Col 13-14; 96pp; English.  
 XX CC The invention relates to new oligonucleotide probes and primers used for  
 CC the detection of human papillomaviruses (HPV) which are not genital types  
 CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used  
 CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The  
 CC primers can be used to detect these HPV types in conjunction with the  
 CC consensus primers and typing probes AAT44733-T44906, which are based on  
 CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV  
 CC sequences. This primer together with the negative strand primers AAT44736  
 CC -7 amplifies a 1.1-1.4 kb region across the L1, URR (transcription  
 CC regulatory region) and E6 regions from HPV types 6, 11, 16, 18 and 33.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 15; DB 2; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGATACCACACGCAG 15  
 DB 8 AGATACCACACGCAG 22  
 RESULT 10  
 AAT77886  
 ID AAT77886 standard; DNA; 25 BP.  
 XX AC AAT77886;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 06-OCT-1997 (first entry)  
 XX DE Human papillomavirus probe FS10.  
 XX KW Human; papillomavirus; HPV; probe; detection; ss.  
 XX OS Synthetic.  
 XX PN US5639871-A.  
 XX PD 17-JUN-1997.  
 XX PF 01-JUN-1995; 95US-00457648.  
 XX PR 09-SEP-1988; 88US-00243486.  
 XX PR 10-MAR-1989; 89US-00322550.  
 XX PR 29-AUG-1989; 89WO-US003747.  
 XX PR 14-NOV-1990; 90US-00613142.

PR 20-APR-1993; 93US-00050743.  
 PR 24-SEP-1993; 93US-00126452.  
 XX (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 XX PI Imprim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;  
 XX PI Gravitt PE;  
 XX WPI; 1997-332084/30.  
 XX DR New oligo:nucleotide probes for human papilloma-virus - used for  
 XX PT detecting and typing HPV and for detecting previously unknown HPV types  
 XX PT and subtypes.  
 XX PS Disclosure; Col 69-70; 94pp; English.  
 XX CC The present sequence is a human papillomavirus (HPV) specific probe.  
 XX CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 XX CC correct PR field.)  
 XX SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 15; DB 2; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGATACCACACGCAG 15  
 DB 8 AGATACCACACGCAG 22  
 RESULT 11  
 AAV17472  
 ID AAV17472 standard; DNA; 25 BP.  
 XX AC AAV17472;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 04-JUN-1998 (first entry)  
 XX DE Primer FS10 for human papillomavirus typing.  
 XX KW Human papillomavirus; HPV; HPV detection; HPV typing;  
 XX KW L1 type-specific probe; PCR primer; ss.  
 XX OS Synthetic.  
 XX OS Human papillomavirus.  
 XX PN US5705627-A.  
 XX PD 06-JAN-1998.  
 XX PF 26-MAY-1995; 95US-00452055.  
 XX PR 09-SEP-1988; 88US-00243486.  
 XX PR 10-MAR-1989; 89US-00322550.  
 XX PR 14-NOV-1990; 90US-00613142.  
 XX PR 20-APR-1993; 93US-00050743.  
 XX PA (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 XX PI Ting Y, Resnick RM, Greer CE, Bauer HM, Manos MM;  
 XX WPI; 1998-192210/17.  
 XX DE Human papilloma probes and primers - useful for, e.g. detecting and  
 XX PT typing of human papilloma viruses.  
 XX PS Disclosure; Col 5-6; 37pp; English.  
 XX CC This sequence represents a human papillomavirus (HPV) L1 type-specific  
 XX CC primer of the invention. This sequence may be used in conjunction with L1  
 XX CC specific probes for detecting and typing HPV. Identification and typing

CC of HPV is important as different types of HPV pose different risks for  
 CC infected individuals. HPV16 and HPV18 have been more consistently  
 CC identified in higher grades of cervical dysplasia and carcinoma than  
 CC other HPV types. (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 25 BP; 7 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 15; DB 2; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGATACCACACGCAG 15  
 |||||  
 Db 8 AGATACCACACGCAG 22

RESULT 12  
 AAQ87034  
 ID AAQ87034 standard; DNA; 26 BP.  
 XX  
 AC AAQ87034;  
 XX  
 DT 12-JAN-1996 (first entry)  
 XX  
 DE Oligonucleotide probe to identify HPV 11 late genes.  
 XX  
 KW probe; hybridisation; human papilloma virus; HPV; detection; riboprobe;  
 KW diagnosis; ss.  
 OS Synthetic.  
 XX  
 PN WO9511316-A1.  
 XX  
 PD 27-APR-1995.  
 XX  
 PF 19-OCT-1994; 94WO-US012044.  
 XX  
 PR 22-OCT-1993; 93US-00141711.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Martin FH, Jacobsen FW, Green CL;  
 XX  
 DR WPI; 1995-193795/25.  
 XX  
 PT Detection of target nucleic acid sequence in biological samples - using a  
 PT labelled riboprobe which hybridises to target nucleic acid for use in  
 PT medical diagnostics, forensics, and research.  
 XX  
 PS Example 1; Page 37; 75pp; English.  
 XX  
 CC The probe was 32P-end labeled and added to a HPV 11 sample to identify  
 CC late genes. Hybridisation was conducted and plaques contg. DNA mols.  
 CC complementary to the probe were identified. The plaques were probed also  
 CC with a probe for early genes (AAQ87035). Positive plaques hybridised to  
 CC both early and late probes. DNA was prep'd. for the prodn. of riboprobes  
 CC to be used in the methods of the invention. Riboprobes improve the  
 CC detection limits of nucleic acid hybridisation. The detection methods  
 CC using riboprobes can be used in medical diagnostics, forensics and  
 CC molecular biology research  
 XX  
 SQ Sequence 26 BP; 8 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 15; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 96;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGATACCACACGCAG 15  
 |||||  
 Db 9 AGATACCACACGCAG 23

RESULT 13

AAT10813  
 ID AAT10813 standard; DNA; 25 BP.  
 XX  
 AC AAT10813;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-APR-1996 (first entry)  
 XX  
 DE Human papilloma virus L1 region consensus probe MY46.  
 XX  
 KW Human papilloma virus; probe; detection; diagnosis; genital; oral;  
 KW carcinomas; research; L1 region; consensus; MY46; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5447839-A.  
 XX  
 PD 05-SEP-1995.  
 XX  
 PF 20-APR-1993; 93US-00050743.  
 XX  
 PR 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 09-SEP-1989; 89WO-US003747.  
 PR 14-NOV-1990; 90US-00613142.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE INC.  
 XX  
 PI Ting Y, Resnick RM, Greer CE, Manos MM, Bauer HM;  
 XX  
 DR WPI; 1995-319884/41.  
 XX  
 PT Detection of human papilloma virus DNA by amplification - using specific  
 PT consensus primer pairs and pref. detection with generic or type specific  
 PT probes for use in research and diagnosis.  
 XX  
 PS Claim 2; Col 33-34; 36pp; English.  
 XX  
 CC A human papilloma virus (HPV) L1 region consensus probe comprising an  
 CC equimolar mix of the probes AAT10812-15, was used to detect HPV for  
 CC research or diagnostic purposes, e.g. to identify HPV that are implicated  
 CC in genital or oral carcinomas. (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX  
 SQ Sequence 25 BP; 6 A; 7 C; 6 G; 5 T; 0 U; 1 Other;  
 Query Match 97.3%; Score 14.6; DB 2; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGATACCACACGCAG 15  
 |||||  
 Db 8 AGATACCACACGCAG 22

RESULT 14  
 AAT44761  
 ID AAT44761 standard; DNA; 25 BP.  
 XX  
 AC AAT44761;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 29-JAN-1997 (first entry)  
 XX  
 DE L1 consensus probe MY46.  
 XX  
 KW Probe; primer; PCR; polymerase chain reaction; amplification;  
 KW human papillomavirus; consensus; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US527898-A.  
 XX

PD 18-JUN-1996.  
 XX 07-JUN-1995; 95US-00474542.  
 XX 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 09-SEP-1989; 89WO-US003747.  
 PR 14-NOV-1990; 90US-00613142.  
 PR 20-APR-1993; 93US-00050743.  
 PR 24-SEP-1993; 93US-00126452.  
 XX (HOFF ) HOFFMANN LA ROCHE INC.  
 XX Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;  
 PI WPI; 1996-299903/30.  
 DR Nucleic acid hybridisation probes - specific for selected human papilloma  
 PT virus types.  
 XX Disclosure; Col 29-30; 96pp; English.  
 XX The invention relates to new oligonucleotide probes and primers used for  
 CC the detection of human papillomaviruses (HPV) which are not genital types  
 CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used  
 CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The  
 CC primers can be used to detect these HPV types in conjunction with the  
 CC consensus primers and typing probes AAT44733-T44906, which are based on  
 CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV  
 CC sequences. Detection of the amplification prods. is done with probes  
 CC derived from consensus sequences found in all characterised HPV  
 CC sequences. The probes AAT44755-61 are examples of L1 consensus probes for  
 CC identifying the amplified products. (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX SQ Sequence 25 BP; 6 A; 7 C; 6 G; 5 T; 0 U; 1 Other;  
 Query Match 97.3%; Score 14.6; DB 2; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGATACCACACGCGAG 15  
 Db 8 AGATACCACACGCGAG 22  
 RESULT 15  
 AAT77893  
 ID AAT77893 standard; DNA; 25 BP.  
 XX AC AAT77893;  
 XX 25-MAR-2003 (revised)  
 DT 06-OCT-1997 (first entry)  
 XX Human papillomavirus probe MY46.  
 DE Human, papillomavirus; HPV; probe; detection; ss.  
 KW Synthetic.  
 XX US5639871-A.  
 PN 17-JUN-1997.  
 XX 01-JUN-1995; 95US-00457648.  
 XX 09-SEP-1988; 88US-00243486.  
 PR 10-MAR-1989; 89US-00322550.  
 PR 29-AUG-1989; 89WO-US003747.  
 PR 14-NOV-1990; 90US-00613142.  
 PR 20-APR-1993; 93US-00050743.  
 PR 24-SEP-1993; 93US-00126452.

XX (HOFF ) ROCHE MOLECULAR SYSTEMS INC.  
 XX Impraim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;  
 PI Gravitt PE;  
 XX WPI; 1997-332084/30.  
 XX New oligo:nucleotide probes for human papilloma-virus - used for  
 PT detecting and typing HPV and for detecting previously unknown HPV types  
 PT and subtypes.  
 XX Disclosure; Col 71-72; 94pp; English.  
 XX The present sequence is a human papillomavirus (HPV) specific probe.  
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 CC correct PR field.)  
 XX SQ Sequence 25 BP; 6 A; 7 C; 6 G; 5 T; 0 U; 1 Other;  
 Query Match 97.3%; Score 14.6; DB 2; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 1.6e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGATACCACACGCGAG 15  
 Db 8 AGATACCACACGCGAG 22  
 Search completed: June 23, 2005, 18:24:36  
 Job time : 421 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 18:05:30 ; Search time 123 Seconds  
(without alignments)  
199.546 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 970836

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:\*
- 1: /cgn2\_6/ptodata/1/ina/5A COMB.seq:\*
  - 2: /cgn2\_6/ptodata/1/ina/5B COMB.seq:\*
  - 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*
  - 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*
  - 5: /cgn2\_6/ptodata/1/ina/PTCUS COMB.seq:\*
  - 6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	25	1	US-08-474-542A-21
2	15	100.0	25	1	US-08-457-648-21
3	14.6	97.3	25	1	US-08-050-743-9
4	14.6	97.3	25	1	US-08-474-542A-28
5	14.6	97.3	25	1	US-08-457-648-28
6	14.6	97.3	25	1	US-08-452-055-9
7	13.4	89.3	25	1	US-08-474-542A-26
8	13.4	89.3	25	1	US-08-474-542A-271
9	13.4	89.3	25	1	US-08-457-648-26
10	13.4	89.3	25	1	US-08-457-648-271
11	13	86.7	21	1	US-07-722-798A-75
12	13	86.7	22	1	US-07-722-798A-76
13	12.4	82.7	25	1	US-08-474-542A-106
14	12.4	82.7	25	1	US-08-457-648-106
15	12.4	82.7	25	3	US-08-155-938-35
16	12.4	82.7	27	3	US-08-155-938-34
17	11.8	78.7	25	1	US-08-474-542A-22
18	11.8	78.7	25	1	US-08-457-648-22
19	11.8	78.7	25	4	US-09-396-196G-57331
20	11.4	76.0	24	4	US-08-899-112B-14
21	11.4	76.0	24	4	US-09-011-553-15
22	11.4	76.0	25	4	US-09-396-196G-14509
23	11.4	76.0	25	4	US-09-396-196G-57330
24	11	73.3	23	3	US-08-338-579A-70
25	11	73.3	23	5	PTC-US94-09851-70
26	10.8	72.0	20	4	US-09-198-452A-6764
27	10.8	72.0	20	4	US-09-033-936-71

c	28	10.8	72.0	24	4	US-09-705-872-8	Sequence 8, Appli
c	29	10.8	72.0	25	4	US-09-396-196G-4231	Sequence 4231, Ap
	30	10.8	72.0	25	4	US-09-396-196G-10749	Sequence 10749, A
	31	10.8	72.0	25	4	US-09-396-196G-10750	Sequence 10750, A
	32	10.8	72.0	25	4	US-09-396-196G-44088	Sequence 44088, A
	33	10.8	72.0	25	4	US-09-396-196G-44089	Sequence 44089, A
	34	10.8	72.0	25	4	US-09-396-196G-54438	Sequence 54438, A
	35	10.8	72.0	25	4	US-09-396-196G-54439	Sequence 54439, A
	36	10.8	72.0	25	4	US-09-396-196G-65875	Sequence 65875, A
	37	10.8	72.0	25	4	US-09-396-196G-88276	Sequence 88276, A
	38	10.8	72.0	25	4	US-09-396-196G-90071	Sequence 90071, A
	39	10.8	72.0	25	4	US-09-396-196G-100045	Sequence 100045, A
	40	10.8	72.0	25	4	US-09-396-196G-100047	Sequence 100047, A
	41	10.8	72.0	25	4	US-09-396-196G-100048	Sequence 100048, A
	42	10.8	72.0	25	4	US-09-396-196G-111377	Sequence 111377, A
	43	10.8	72.0	25	4	US-09-396-196G-111378	Sequence 111378, A
	44	10.8	72.0	25	4	US-09-396-196G-111394	Sequence 111394, A
	45	10.8	72.0	25	4	US-09-396-196G-111395	Sequence 111395, A

## ALIGNMENTS

RESULT 1  
US-08-474-542A-21  
; Sequence 21, Application US/08474542A  
; Patent No. 5527898  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, Heidi M.  
; APPLICANT: Gravitt, Patti E.  
; APPLICANT: Greer, Catherine E.  
; APPLICANT: Imprim, Chaka C.  
; APPLICANT: Manos, M. Michele  
; APPLICANT: Resnick, Robert M.  
; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 298  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,542A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 9234  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-474-542A-21

Query Match 100.0%; Score 15; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGATACCACGCAG 15
Db 8 AGATACCACGCAG 22

RESULT 2
US-08-457-648-21
; Sequence 21, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-457-648-21

Query Match 100.0%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACGCAG 15
Db 8 AGATACCACGCAG 22

RESULT 3
US-08-050-743-9
; Sequence 9, Application US/08050743
; Patent No. 5447839
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Manos, Michele
; APPLICANT: Resnick, Robert M.
; APPLICANT: Ting, Yi
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 85
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,743
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-050-743-9

Query Match 97.3%; Score 14.6; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGATACCACGCAG 15
Db 8 AGATACCACGCAG 22

RESULT 4
US-08-474-542A-28
; Sequence 28, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
```

REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 9234  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-474-542A-28

Query Match 97.3%; Score 14.6; DB 1; Length 25;  
Best Local Similarity 93.3%; Pred. No. 40;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACGCGAG 15  
|||||:|||||  
Db 8 AGATACCACGCGAG 22

RESULT 5  
US-08-457-648-28  
; Sequence 28, Application US/08457648  
; Patent No. 5639871  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, Heidi M.  
; APPLICANT: Gravitt, Patti E.  
; APPLICANT: Greer, Catherine E.  
; APPLICANT: Imprim, Chaka C.  
; APPLICANT: Manos, M. Michele  
; APPLICANT: Resnick, Robert M.  
; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 298  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/457,648  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 9205  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2977  
; TELEFAX: (510) 814-2974  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-457-648-28

Query Match 97.3%; Score 14.6; DB 1; Length 25;  
Best Local Similarity 93.3%; Pred. No. 40;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACGCGAG 15  
|||||:|||||  
Db 8 AGATACCACGCGAG 22

RESULT 6  
US-08-452-055-9  
; Sequence 9, Application US/08452055  
; Patent No. 5705627  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, Heidi M.  
; APPLICANT: Greer, Catherine E.  
; APPLICANT: Manos, Michele  
; APPLICANT: Resnick, Robert M.  
; APPLICANT: Ting, Yi  
; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 85  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/452,055  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sias, Stacey R.  
; REGISTRATION NUMBER: 32,630  
; REFERENCE/DOCKET NUMBER: 9188  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2863  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-452-055-9

Query Match 97.3%; Score 14.6; DB 1; Length 25;  
Best Local Similarity 93.3%; Pred. No. 40;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACGCGAG 15  
|||||:|||||  
Db 8 AGATACCACGCGAG 22

RESULT 7  
US-08-474-542A-26  
; Sequence 26, Application US/08474542A  
; Patent No. 5527898  
; GENERAL INFORMATION:  
; APPLICANT: Bauer, Heidi M.  
; APPLICANT: Gravitt, Patti E.  
; APPLICANT: Greer, Catherine E.  
; APPLICANT: Imprim, Chaka C.  
; APPLICANT: Manos, M. Michele  
; APPLICANT: Resnick, Robert M.  
; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 298

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,542A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-474-542A-26

Query Match      89.3%; Score 13.4; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACACGCAG 15
Db      8 AGATACCACACGTA 22

RESULT 8
US-08-474-542A-271
Sequence 271, Application US/08474542A
Patent No. 5527898
GENERAL INFORMATION:
APPLICANT: Bauer, Heidi M.
APPLICANT: Gravitt, Patti E.
APPLICANT: Greer, Catherine E.
APPLICANT: Impraim, Chaka C.
APPLICANT: Manos, M. Michele
APPLICANT: Resnick, Robert M.
TITLE OF INVENTION: Detection of Human Papillomavirus by the
NUMBER OF SEQUENCES: 298
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,542A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.

```

```

REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 271:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-474-542A-271

Query Match      89.3%; Score 13.4; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACACGCAG 15
Db      8 AGATACCACACGCGAG 22

RESULT 9
US-08-457-648-26
Sequence 26, Application US/08457648
Patent No. 5639871
GENERAL INFORMATION:
APPLICANT: Bauer, Heidi M.
APPLICANT: Gravitt, Patti E.
APPLICANT: Greer, Catherine E.
APPLICANT: Impraim, Chaka C.
APPLICANT: Manos, M. Michele
APPLICANT: Resnick, Robert M.
TITLE OF INVENTION: Detection of Human Papillomavirus by the
NUMBER OF SEQUENCES: 298
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,648
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-457-648-26

Query Match      89.3%; Score 13.4; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 AGATACCACGCGAG 15  
 Db 8 AGATACCACGCGTAG 22

RESULT 10

US-08-457-648-271  
 ; Sequence 271, Application US/08457648  
 ; Patent No. 5639871  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bauer, Heidi M.  
 ; APPLICANT: Gravit, Patti E.  
 ; APPLICANT: Greer, Catherine E.  
 ; APPLICANT: Impra, Chaka C.  
 ; APPLICANT: Manos, M. Michele  
 ; APPLICANT: Resnick, Robert M.  
 ; TITLE OF INVENTION: Detection of Human Papillomavirus by the  
 ; TITLE OF INVENTION: Polymerase Chain Reaction  
 ; NUMBER OF SEQUENCES: 298  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffmann-La Roche Inc.  
 ; STREET: 340 Kingsland Street  
 ; CITY: Nutley  
 ; STATE: New Jersey  
 ; COUNTRY: U.S.A.  
 ; ZIP: 07110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/457,648  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Petry, Douglas A.  
 ; REGISTRATION NUMBER: 35,321  
 ; REFERENCE/DOCKET NUMBER: 9205  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (510) 814-2974  
 ; TELEFAX: (510) 814-2977  
 ; INFORMATION FOR SEQ ID NO: 271:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 25 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-457-648-271

Query Match 89.3%; Score 13.4; DB 1; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 2e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGATACCACGCGAG 15  
 Db 8 AGATACCACGCGAG 22

RESULT 11

US-07-722-798A-75  
 ; Sequence 75, Application US/07722798A  
 ; Patent No. 5427930  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Larry G. Birkenmeyer  
 ; APPLICANT: John J. Carrino  
 ; APPLICANT: Bruce J. Dille  
 ; APPLICANT: Hsiang-Yun Hu  
 ; APPLICANT: Jon David Kratochvil  
 ; APPLICANT: Thomas G. Laffler  
 ; APPLICANT: Ronald L. Marshall  
 ; APPLICANT: Laurie A. Rinehardt

APPLICANT: Natalie A. Solomon  
 TITLE OF INVENTION: AMPLIFICATION OF TARGET NUCLEIC  
 TITLE OF INVENTION: ACIDS USING GAP FILLING LIGASE CHAIN REACTION  
 NUMBER OF SEQUENCES: 124  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: One Abbott Park Road  
 CITY: Abbott Park  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy diskette  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Wordperfect 5.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/722,798A  
 FILING DATE: 19910628  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Thomas D. Brainard  
 REGISTRATION NUMBER: 32,459  
 REFERENCE/DOCKET NUMBER: 4773.US.P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 708-937-4884  
 TELEFAX: 708-937-9556  
 INFORMATION FOR SEQ ID NO: 75:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 21  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Other nucleic acid (synthetic DNA)  
 US-07-722-798A-75

Query Match 86.7%; Score 13; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATACCACGCA 14  
 Db 9 GATACCACGCA 21

RESULT 12

US-07-722-798A-76/c  
 ; Sequence 76, Application US/07722798A  
 ; Patent No. 5427930  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Larry G. Birkenmeyer  
 ; APPLICANT: John J. Carrino  
 ; APPLICANT: Bruce J. Dille  
 ; APPLICANT: Hsiang-Yun Hu  
 ; APPLICANT: Jon David Kratochvil  
 ; APPLICANT: Thomas G. Laffler  
 ; APPLICANT: Ronald L. Marshall  
 ; APPLICANT: Laurie A. Rinehardt  
 ; APPLICANT: Natalie A. Solomon  
 TITLE OF INVENTION: AMPLIFICATION OF TARGET NUCLEIC  
 TITLE OF INVENTION: ACIDS USING GAP FILLING LIGASE CHAIN REACTION  
 NUMBER OF SEQUENCES: 124  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: One Abbott Park Road  
 CITY: Abbott Park  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy diskette  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Wordperfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/722,798A
; FILING DATE: 19910628
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas D. Brainard
; REGISTRATION NUMBER: 32,459
; REFERENCE/DOCKET NUMBER: 4773.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-4884
; TELEFAX: 708-937-9556
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid (synthetic DNA)
US-07-722-798A-76

Query Match      86.7%; Score 13; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GATACCAACGCGCA 14
      |||||
Db      13 GATACCAACGCGCA 1

RESULT 13
US-08-474-542A-106
; Sequence 106, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-474-542A-106

Query Match      82.7%; Score 12.4; DB 1; Length 25;
Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; MOLECULE TYPE: DNA (genomic)
US-08-474-542A-106

Query Match      82.7%; Score 12.4; DB 1; Length 25;
Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GATACCAACGCGCGAG 15
      |||||
Db      9 GATACCAACGCGCGAG 22

RESULT 14
US-08-457-648-106
; Sequence 106, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-457-648-106

Query Match      82.7%; Score 12.4; DB 1; Length 25;
Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GATACCAACGCGCGAG 15
      |||||
Db      9 GATACCAACGCGCGAG 22

RESULT 15
US-08-155-938-35
; Sequence 35, Application US/08155938
; Patent No. 6004826
; GENERAL INFORMATION:
; APPLICANT: Segev, David
```

TITLE OF INVENTION: PROCESS FOR AMPLIFYING AND DETECTING  
 NUCLEIC ACID SEQUENCES  
 NUMBER OF SEQUENCES: 42  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ImClone Systems Incorporated  
 STREET: 180 Varlick Street  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10014  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/155,938  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/841,649  
 FILING DATE:  
 APPLICATION NUMBER: US 07/221,750  
 FILING DATE: 20-JUL-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/784,749  
 FILING DATE: 28-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Feit, Irving N.  
 REGISTRATION NUMBER: 28,601  
 REFERENCE/DOCKET NUMBER: SEG-1-CP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-645-1405  
 TELEFAX: 212-645-2054  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-155-938-35

Query Match 82.7%; Score 12.4; DB 3; Length 25;  
 Best Local Similarity 92.9%; Pred. No. 7.7e+02;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GATACACACGAG 15  
 |||||  
 Db 9 GATACACACGAG 22

Search completed: June 23, 2005, 19:44:46  
 Job time : 124 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 18:17:36 ; Search time 520 Seconds  
(without alignments)  
180.303 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 5576672

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA:\*
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  - 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
  - 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
  - 22: /cgn2\_6/ptodata/1/pubpna/US10J\_PUBCOMB.seq:\*
  - 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
  - 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
  - 25: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
  - 26: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
  - 27: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	9	US-09-825-482-6
2	15	100.0	15	15	US-10-323-188-6
3	15	100.0	15	15	US-10-286-387-23
4	15	100.0	17	9	US-09-825-482-7
5	15	100.0	17	15	US-10-323-188-7
6	15	100.0	17	15	US-10-286-387-24
7	15	100.0	22	9	US-09-825-482-9

8	15	100.0	22	15	US-10-323-188-9	Sequence 9, Appli
9	15	100.0	22	15	US-10-286-387-26	Sequence 26, Appli
10	13.4	89.3	25	21	US-10-719-900-842484	Sequence 842484,
11	13.4	89.3	25	21	US-10-719-900-882687	Sequence 882687,
12	13.4	89.3	25	21	US-10-719-900-964593	Sequence 964593,
13	12.4	82.7	14	9	US-09-825-482-3	Sequence 3, Appli
14	12.4	82.7	14	15	US-10-323-188-3	Sequence 3, Appli
15	12.4	82.7	14	15	US-10-286-387-3	Sequence 3, Appli
16	12.4	82.7	25	15	US-10-098-263B-70330	Sequence 70330, A
17	12.4	82.7	25	15	US-10-719-900-1035	Sequence 1035, Ap
18	12.4	82.7	25	21	US-10-719-900-45007	Sequence 45007, A
19	12.4	82.7	25	21	US-10-719-900-45008	Sequence 45008, A
20	12.4	82.7	25	21	US-10-719-900-501938	Sequence 501938,
21	12.4	82.7	25	21	US-10-719-900-707395	Sequence 707395,
22	12.4	82.7	25	21	US-10-719-900-768545	Sequence 768545,
23	12.4	82.7	25	21	US-10-956-157-68055	Sequence 68055, A
24	12.4	82.7	25	21	US-10-956-157-126114	Sequence 126114,
25	12	80.0	25	21	US-10-719-900-463970	Sequence 463970,
26	12	80.0	25	21	US-10-719-900-463971	Sequence 463971,
27	12	80.0	25	21	US-10-719-900-857602	Sequence 857602,
28	11.8	78.7	15	9	US-09-825-482-8	Sequence 8, Appli
29	11.8	78.7	15	15	US-10-323-188-8	Sequence 8, Appli
30	11.8	78.7	15	15	US-10-286-387-25	Sequence 25, Appl
31	11.8	78.7	20	19	US-10-361-002-34	Sequence 34, Appl
32	11.8	78.7	20	19	US-10-361-004-34	Sequence 34, Appl
33	11.8	78.7	25	21	US-10-719-900-12909	Sequence 12909, A
34	11.8	78.7	25	21	US-10-719-900-46150	Sequence 46150, A
35	11.8	78.7	25	21	US-10-719-900-97970	Sequence 97970, A
36	11.8	78.7	25	21	US-10-719-900-99463	Sequence 99463, A
37	11.8	78.7	25	21	US-10-719-900-158555	Sequence 158555,
38	11.8	78.7	25	21	US-10-719-900-158567	Sequence 158567,
39	11.8	78.7	25	21	US-10-719-900-167555	Sequence 167555,
40	11.8	78.7	25	21	US-10-719-900-207951	Sequence 207951,
41	11.8	78.7	25	21	US-10-719-900-224387	Sequence 224387,
42	11.8	78.7	25	21	US-10-719-900-229611	Sequence 229611,
43	11.8	78.7	25	21	US-10-719-900-229612	Sequence 229612,
44	11.8	78.7	25	21	US-10-719-900-276617	Sequence 276617,
45	11.8	78.7	25	21	US-10-719-900-388065	Sequence 388065,

## ALIGNMENTS

### RESULT 1

US-09-825-482-6 Application US/09825482  
; Patent No. US20020155427A1  
; GENERAL INFORMATION:  
; APPLICANT: Lentricchia, Brian  
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes  
; FILE REFERENCE: CVM-035  
; CURRENT APPLICATION NUMBER: US/09/825,482  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/194,304  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: US 60/225,524  
; PRIOR FILING DATE: 2000-08-15  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PNA Probe VI  
US-09-825-482-6

Query Match 100.0%; Score 15; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QV 1 AGATACCACACGCAG 15

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Db      1 AGATACCACACGCAG 15
|||||
RESULT 2
US-10-323-188-6
; Sequence 6, Application US/10323188
; Publication No. US20030108866A1
; GENERAL INFORMATION:
; APPLICANT: Cohenford, Menashi
; APPLICANT: Lentrichia, Brian
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035DV
; CURRENT APPLICATION NUMBER: US/10/323,188
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 09/825,482
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,304
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/225,524
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA Probe VI
US-10-323-188-6
Query Match      100.0%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGATACCACACGCAG 15
|||||
Db      1 AGATACCACACGCAG 15
|||||
RESULT 3
US-10-286-387-23
; Sequence 23, Application US/10286387
; Publication No. US20030143529A1
; GENERAL INFORMATION:
; APPLICANT: Cytec Corporation
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035CP
; CURRENT APPLICATION NUMBER: US/10/286,387
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-286-387-23
Query Match      100.0%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGATACCACACGCAG 15
|||||
Db      1 AGATACCACACGCAG 15
|||||
RESULT 4
US-09-825-482-7
; Sequence 7, Application US/09825482
; Patent No. US20020155427A1
; GENERAL INFORMATION:
; APPLICANT: Cohenford, Menashi
; APPLICANT: Lentrichia, Brian
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035
; CURRENT APPLICATION NUMBER: US/09/825,482
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,304
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/225,524
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA Probe VII
US-09-825-482-7
Query Match      100.0%; Score 15; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGATACCACACGCAG 15
|||||
Db      2 AGATACCACACGCAG 16
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RESULT 5
US-10-323-188-7
; Sequence 7, Application US/10323188
; Publication No. US20030108866A1
; GENERAL INFORMATION:
; APPLICANT: Cohenford, Menashi
; APPLICANT: Lentrichia, Brian
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035DV
; CURRENT APPLICATION NUMBER: US/10/323,188
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 09/825,482
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,304
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/225,524
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA Probe VII
US-10-323-188-7
Query Match      100.0%; Score 15; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AGATACCACACGCAG 15
|||||
Db      2 AGATACCACACGCAG 16
|||||
RESULT 6
US-10-286-387-24
; Sequence 24, Application US/10286387
; Publication No. US20030143529A1
; GENERAL INFORMATION:
; APPLICANT: Cytec Corporation
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes

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FILE REFERENCE: cym-035CP  
 CURRENT APPLICATION NUMBER: US/10/286,387  
 CURRENT FILING DATE: 2003-02-28  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 24  
 LENGTH: 17  
 TYPE: DNA  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: PNA probe  
 US-10-286-387-24

Query Match 100.0%; Score 15; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 89;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15  
 Db 2 AGATACCACACGCAG 16

RESULT 7  
 US-09-825-482-9  
 Sequence 9, Application US/09825482  
 Patent No. US20020155427A1  
 GENERAL INFORMATION:  
 APPLICANT: Cohenford, Menashi  
 APPLICANT: Lentricchia, Brian  
 TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes  
 FILE REFERENCE: Cym-035  
 CURRENT APPLICATION NUMBER: US/09/825,482  
 CURRENT FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: US 60/194,304  
 PRIOR FILING DATE: 2000-04-03  
 PRIOR APPLICATION NUMBER: US 60/225,524  
 PRIOR FILING DATE: 2000-08-15  
 NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 9  
 LENGTH: 22  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: MC01 HPV consensus primer sequence  
 US-09-825-482-9

Query Match 100.0%; Score 15; DB 9; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15  
 Db 7 AGATACCACACGCAG 21

RESULT 8  
 US-10-323-188-9  
 Sequence 9, Application US/1023188  
 Publication No. US20030108866A1  
 GENERAL INFORMATION:  
 APPLICANT: Cohenford, Menashi  
 APPLICANT: Lentricchia, Brian  
 TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes  
 FILE REFERENCE: Cym-035DV  
 CURRENT APPLICATION NUMBER: US/10/323,188  
 CURRENT FILING DATE: 2002-12-18  
 PRIOR APPLICATION NUMBER: 09/825,482  
 PRIOR FILING DATE: 2001-04-03  
 PRIOR APPLICATION NUMBER: US 60/194,304  
 PRIOR FILING DATE: 2000-04-03  
 PRIOR APPLICATION NUMBER: US 60/225,524  
 PRIOR FILING DATE: 2000-08-15

NUMBER OF SEQ ID NOS: 11  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 9  
 LENGTH: 22  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: MC01 HPV consensus primer sequence  
 US-10-323-188-9

Query Match 100.0%; Score 15; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15  
 Db 7 AGATACCACACGCAG 21

RESULT 9  
 US-10-286-387-26  
 Sequence 26, Application US/10286387  
 Publication No. US20030143529A1  
 GENERAL INFORMATION:  
 APPLICANT: Cytoc Corporation  
 TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes  
 FILE REFERENCE: cym-035CP  
 CURRENT APPLICATION NUMBER: US/10/286,387  
 CURRENT FILING DATE: 2003-02-28  
 NUMBER OF SEQ ID NOS: 31  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 26  
 LENGTH: 22  
 TYPE: DNA  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: Modified consensus primer for amplifying multiple HPV strains  
 US-10-286-387-26

Query Match 100.0%; Score 15; DB 15; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 90;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15  
 Db 7 AGATACCACACGCAG 21

RESULT 10  
 US-10-719-900-842484  
 Sequence 842484, Application US/10719900  
 Publication No. US20050026164A1  
 GENERAL INFORMATION:  
 APPLICANT: Xue Mei  
 TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
 FILE REFERENCE: 3528.1  
 CURRENT APPLICATION NUMBER: US/10/719,900  
 CURRENT FILING DATE: 2003-11-20  
 PRIOR APPLICATION NUMBER: 60/427,808  
 PRIOR FILING DATE: 2002-11-20  
 NUMBER OF SEQ ID NOS: 982914  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 SEQ ID NO 842484  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-10-719-900-842484

Query Match 89.3%; Score 13.4; DB 21; Length 25;  
 Best Local Similarity 93.3%; Pred. No. 7.7e+02;  
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGATACCACACGCAG 15

```
Db      8 AGATACCACGCGAG 22
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RESULT 11
US-10-719-900-882687
; Sequence 882687, Application US/10719900
; Publication No. US2005002616A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 882687
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-882687

Query Match      89.3%; Score 13.4; DB 21; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACGCGAG 15
|||||
Db      8 AGATACCACGCCAG 22
|||||

RESULT 12
US-10-719-900-964593
; Sequence 964593, Application US/10719900
; Publication No. US2005002616A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 964593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-964593

Query Match      89.3%; Score 13.4; DB 21; Length 25;
Best Local Similarity 93.3%; Pred. No. 7.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AGATACCACGCGAG 15
|||||
Db      4 AGATAACACGCGAG 18
|||||

RESULT 13
US-09-825-482-3
; Sequence 3, Application US/09825482
; Patent No. US20020155427A1
; GENERAL INFORMATION:
; APPLICANT: Cohenford, Menashi
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035
; CURRENT APPLICATION NUMBER: US/09/825,482
; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: US 60/194,304
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/225,524
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA Probe III
US-10-323-188-3

Query Match      82.7%; Score 12.4; DB 15; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GATACCACGCGAG 15
|||||
Db      1 GATACCACGCGAG 14
|||||

RESULT 14
US-10-323-188-3
; Sequence 3, Application US/10323188
; Publication No. US20030108866A1
; GENERAL INFORMATION:
; APPLICANT: Cohenford, Menashi
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035DV
; CURRENT APPLICATION NUMBER: US/10/323,188
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 09/825,482
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,304
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/225,524
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PNA Probe III
US-10-323-188-3

Query Match      82.7%; Score 12.4; DB 15; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GATACCACGCGAG 15
|||||
Db      1 GATACCACGCGAG 14
|||||

RESULT 15
US-10-286-387-3
; Sequence 3, Application US/10286387
; Publication No. US20030143529A1
; GENERAL INFORMATION:
; APPLICANT: Cytoc Corporation
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: CYM-035CP
; CURRENT APPLICATION NUMBER: US/10/286,387
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 14
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; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-286-387-3
Query Match      82.7%  Score 12.4; DB 15; Length 14;
Best Local Similarity 92.9%  Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy .      2 GATACCAACGCGAG 15
      |||||
Db      1 GATACCACTCGCGAG 14

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Job time : 521 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 17:50:22 ; Search time 2981 Seconds  
(without alignments)  
191.534 Million cell updates/sec

Title: US-09-825-482-6

Perfect score: 15

Sequence: 1 agataccacacgcag 15

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 46888

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

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- 2: gb\_est2.\*
- 3: gb\_hcc.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gsl.\*
- 9: gb\_gsl2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	10.8	72.0	24	7	L32033	L32033 HUMXP11B6B
2	10.4	69.3	24	8	AZ794953	AZ794953 2M0048N21
3	10.4	69.3	26	8	BH792752	BH792752 SALK_0649
4	10.4	69.3	30	9	BX896975	BX896975 Arabidops
C 5	10	66.7	20	8	AZ782314	AZ782314 2M0022D03
6	10	66.7	22	9	AZ782314	AL476402 T. brucei
7	10	66.7	23	9	TA205F05Q	AL490295 T. brucei
C 8	10	66.7	25	1	AI664044	AI664044 ue73e05.r
C 9	9.8	65.3	20	8	AZ770749	AZ770749 IM0572B01
10	9.4	62.7	20	8	AZ307506	AZ307506 IM0009I16
11	9.4	62.7	22	8	AZ346725	AZ346725 IM0082P06
12	9.4	62.7	28	1	AI613292	AI613292 ty35g02.x
13	9.2	61.3	20	8	AZ832127	AZ832127 2M0112M17
C 14	9.2	61.3	21	8	AZ510254	AZ510254 IM0354F10
C 15	9.2	61.3	22	8	AZ309912	AZ309912 IM0017P15
C 16	9.2	61.3	23	8	AZ501123	AZ501123 IM0339A22
17	9.2	61.3	25	1	AI024239	AI024239 ov71g02.s
18	9.2	61.3	27	1	AU010622	AU010622 AU010622
C 19	9.2	61.3	27	8	AZ779966	AZ779966 2M0016C21
C 20	9.2	61.3	27	9	AG190440	AG190440 Pan trogl
21	9.2	61.3	28	1	AA912344	AA912344 ol97h02.s
22	9.2	61.3	28	7	CO784963	CO784963 BL282A.F1
C 23	9.2	61.3	29	8	AZ956741	AZ956741 2M0223C24
24	9.2	61.3	30	8	AZ348488	AZ348488 1M0085L06

C 25	9.2	61.3	30	8	AZ588091	AZ588091 1M0396K03
C 26	9.2	61.3	30	9	CL523751	CL523751 DAL5G03.F
27	9	60.0	20	8	AZ628029	AZ628029 1M0476F17
28	9	60.0	24	8	AZ812858	AZ812858 2M0079B21
C 29	9	60.0	25	8	AZ872633	AZ872633 2M0186K01
30	9	60.0	26	8	AZ435264	AZ435264 1M0222G12
31	9	60.0	28	1	AI037937	AI037937 ox53all.x
C 32	8.8	58.7	19	8	AZ651803	AZ651803 1M0522N11
33	8.8	58.7	20	8	AZ776456	AZ776456 2M0010O03
C 34	8.8	58.7	21	8	AZ769838	AZ769838 1M0570H22
35	8.8	58.7	22	8	AZ603366	AZ603366 1M0422L17
C 36	8.8	58.7	23	8	AZ762598	AZ762598 1M0557I12
37	8.8	58.7	23	8	AZ844618	AZ844618 2M0144M03
C 38	8.8	58.7	24	8	AZ514503	AZ514503 1M0361J19
C 39	8.8	58.7	24	9	AG201951	AG201951 Pan trogl
C 40	8.8	58.7	24	9	TA181A05Q	TA181A05Q T. brucei
41	8.8	58.7	25	1	AI720628	AI720628 ae70g12.x
C 42	8.8	58.7	25	9	TA283B04P	TA283B04P T. brucei
C 43	8.8	58.7	26	8	AZ654939	AZ654939 1M0529N04
C 44	8.8	58.7	26	8	AZ771925	AZ771925 1M0574P19
C 45	8.8	58.7	26	8	AZ941927	AZ941927 2M0201D24

## ALIGNMENTS

RESULT 1  
L32033/c  
LOCUS HUMXP11B6B Human placenta Homo sapiens cDNA clone XP11B6B, mRNA  
DEFINITION sequence.  
ACCESSION L32033  
VERSION L32033.1 GI:927075  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Lee, C.-C., Yazdani, A., Wehnert, M., Bailey, J., Couch, L., Xiong, M., Coolbaugh, M.I., Chinault, C.A., Baldini, A., Lindsay, E.A., Zhao, Z.-Y. and Caskey, C.T.H.  
TITLE Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries  
JOURNAL Hum. Mol. Genet. 4, 1373-1380 (1995)  
MEDLINE 95090257  
PUBMED 7581376  
COMMENT Contact: Caskey, C.T.H.  
FEATURES  
Location/Qualifiers  
source 1..24  
organism="Homo sapiens"  
mol\_type="mRNA"  
db\_xref="taxon:9606"  
map="Xp11.2"  
clone="XP11B6B"  
/clone lib="Human placenta"  
/note="Arrayed cDNAs and cosmid libraries from human placental tissue"

Query Match 72.0%; Score 10.8; DB 7; Length 24;  
Best Local Similarity 85.7%; Pred. No. 2.1e+05;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AGATACCACGCA 14  
||| ||||| |||||  
Db 19 AGAAACCAAGGCA 6

RESULT 2  
AZ794953  
LOCUS 2M0048N21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION linear GSS 16-FEB-2001

clone UUGC2M0048N21 R, genomic survey sequence.

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ACCESSION  A2794953
VERSION     A2794953.1  GI:12941458
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus

REFERENCE   1  (bases 1 to 24)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0048 row: N column: 21
            Seq primer: CACACGAGAACACTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.

FEATURES             source
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        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC2M0048N21"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UGCLM library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptored DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptored mouse DNA was annealed to
            adaptored vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

ORIGIN
    Query Match      69.3%; Score 10.4; DB 8; Length 24;
    Best Local Similarity 91.7%; Pred. No. 3.5e+05;
    Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  AGATACCACACG 12
    ||| |||||
Db   1  AGAGACCACACG 12

RESULT 3
BH792752
LOCUS     BH792752          26 bp      DNA      linear      GSS 02-APR-2002
DEFINITION SALK_064997.35.25.x Arabidopsis thaliana T-DNA insertion lines

ACCESSION  A2794953
VERSION     A2794953.1  GI:12941458
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus

REFERENCE   1  (bases 1 to 24)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0048 row: N column: 21
            Seq primer: CACACGAGAACACTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.

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        /mol_type="genomic DNA"
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        /db_xref="taxon:10090"
        /clone="UUGC2M0048N21"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UGCLM library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptored DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptored mouse DNA was annealed to
            adaptored vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

ORIGIN
    Query Match      69.3%; Score 10.4; DB 8; Length 24;
    Best Local Similarity 91.7%; Pred. No. 3.5e+05;
    Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  AGATACCACACG 12
    ||| |||||
Db   1  AGAGACCACACG 12

RESULT 3
BH792752
LOCUS     BH792752          26 bp      DNA      linear      GSS 02-APR-2002
DEFINITION SALK_064997.35.25.x Arabidopsis thaliana T-DNA insertion lines

```

```

Arabidopsis thaliana genomic clone SALK_064997.35.25.x, genomic
survey sequence.
BH792752    BH792752.1  GI:19889882
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana

REFERENCE   1  (bases 1 to 26)
AUTHORS     Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
            Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
            Shinn, P., Zimmerman, J. and Ecker, J.R.
TITLE       A Sequence-indexed Library of Insertion Mutations in the
            Arabidopsis Genome
JOURNAL     Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGNAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            T-DNA.
            Class: T-DNA tagged.
            Location/Qualifiers
                1..26
                    /organism="Arabidopsis thaliana"
                    /mol_type="genomic DNA"
                    /ecotype="Col-0"
                    /db_xref="taxon:3702"
                    /clone="SALK_064997.35.25.x"
                    /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                    /note="PCR was performed on Arabidopsis thaliana lines
                        each of which contains one or more T-DNA insertion
                        elements. The resultant fragment for each line was
                        directly sequenced to determine the genomic sequence at
                        the site of insertion. Details of the protocols used can
                        be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
    Query Match      69.3%; Score 10.4; DB 8; Length 26;
    Best Local Similarity 91.7%; Pred. No. 3.5e+05;
    Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  AGATACCACACG 12
    ||| |||||
Db   8  AGATTCACACG 19

RESULT 4
BX896975
LOCUS     BX896975          30 bp      DNA      linear      GSS 05-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-764A02-024030,
            genomic survey sequence.
ACCESSION  BX896975
VERSION     BX896975.1  GI:39929470
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana

REFERENCE   1
AUTHORS     Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B.
            CABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
JOURNAL     Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE     22755829
PUBMED      12874060

```

2 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weishaar,B.  
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics  
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)  
MEDLINE 23117147  
PUBMED 14756321

3 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weishaar,B.  
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines  
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)  
PUBMED 14682050

4 (bases 1 to 30)  
Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.  
Direct Submission  
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At1g03300.  
Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
source  
Location/Qualifiers  
1..30  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-76A02-024030"  
/clone.lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Col-0"  
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGAB1 (GenBank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN  
Query Match 69.3%; Score 10.4; DB 9; Length 30;  
Best Local Similarity 91.7%; Pred. No. 3.6e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGATACCACAG 12  
Db 15 AGATACCACAG 26

RESULT 5  
AZ782314/c  
LOCUS AZ782314 20 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0022D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0022D03 R, genomic survey sequence.  
ACCESSION AZ782314  
VERSION AZ782314.1 GI:12915912  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
REFERENCE 1  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0022 row: D column: 03  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0022D03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone.lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
Query Match 66.7%; Score 10; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.9e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCACACGACG 15  
Db 15 CCACACGACG 6

RESULT 6  
TA205F05Q  
LOCUS TA205F05Q 22 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 205f05, reverse sequence, genomic survey sequence.  
ACCESSION AL476402  
VERSION AL476402.1 GI:11843069  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
1 (bases 1 to 22)  
REFERENCE 1  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
Direct Submission  
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrellesanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

1. .22

/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clones="205f05"

## ORIGIN

Query Match 66.7%; Score 10; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ACCACACGCA 14

Db 13 ACCACACGCA 22

## RESULT 7

TA313C04P

LOCUS

DEFINITION T. brucei sheared genomic DNA clone 313c04, forward sequence,  
genomic survey sequence.

ACCESSION

AL490295

VERSION

AL490295.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Constructured at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

1. .23

/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clones="313c04"

## ORIGIN

Query Match 66.7%; Score 10; DB 9; Length 23;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GATACCACAC 11

Db 2 GATACCACAC 11

## RESULT 8

AI664044/c

LOCUS

DEFINITION ue73805.r1 Soares NMPu Mus musculus cDNA clone IMAGE:1496768 5' similar to SW:CHHC\_BOMMO P20730 CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR ; mRNA sequence.

ACCESSION

AI664044

VERSION

AI664044.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
This clone is available royalty-free through LML; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MGI:934372

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m13 rev2 BT from Amersham

High quality sequence stop: 1.

## FEATURES

source

1. .25

/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1496768"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Soares NMPu"  
/notes="Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 66.7%; Score 10; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

Qy 5 ACCACACGCA 14  
Db 25 ACCACACGCA 16

## RESULT 9

AZ770749/c

LOCUS

DEFINITION A2770749 Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0572B01 R, genomic survey sequence.

ACCESSION

A2770749

**VERSION** AZ770749.1 GI:12892278  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
**REFERENCE** Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**AUTHORS** 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0572 row: B column: 01  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.  
**FEATURES** Location/Qualifiers  
 source  
 1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0572B01"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
**ORIGIN**  
 Query Match 65.3%; Score 9.8; DB 8; Length 20;  
 Best Local Similarity 84.6%; Pred. No. 7.7e+05;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 ATACCACAGCAG 15  
 | ||||| |||||  
 Db 13 ACACCAAGCAG 1  
**RESULT 10**  
 AZ307506  
 LOCUS  
 DEFINITION  
 clone UUGC1M0009116 F, genomic survey sequence.  
 accession  
 AZ307506

**VERSION** AZ307506.1 GI:10346574  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
**REFERENCE** Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**AUTHORS** 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0009 row: I column: 16  
 Seq primer: CGTTGTAACACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
**FEATURES** Location/Qualifiers  
 source  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0009116"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
**ORIGIN**  
 Query Match 62.7%; Score 9.4; DB 8; Length 20;  
 Best Local Similarity 90.9%; Pred. No. 1.3e+06;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 ACCACAGCAG 15  
 | ||||| |||||  
 Db 9 ACCACACAG 19  
**RESULT 11**  
 AZ346725  
 LOCUS  
 DEFINITION  
 clone UUGC1M0082P06 F, genomic survey sequence.  
 accession  
 AZ346725

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VERSION      AZ346725.1  GI:10425962
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE    1 (bases 1 to 22)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 22)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: gdunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0082 row: P column: 06
              Seq primer: CGTGTAAACGACGCGCAGT
              Class: plasmid ends
              High quality sequence stop: 22.
              Location/Qualifiers
                1..22
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                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clones="UGC1M0082P06"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UGC1M library"
                  /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high molar excess. The
                    adaptor DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptor mouse DNA was annealed to
                    adaptor vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."

ORIGIN
Query Match      62.7%; Score 9.4; DB 8; Length 22;
Best Local Similarity 90.9%; Pred. No. 1.3e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGATACCAC 11
    ||| |||||
Db 8 AGACACCAC 18

RESULT 12
LOCUS      A1613292
DEFINITION ty35g02.x1 NCI_CGAP UC-2 Homo sapiens cDNA clone IMAGE:2281106 3'
           similar to TR:Q33563 Q33563 BATRO 164 KINETOPLAST ;contains element
           MSR1 repetitive element ;, mRNA sequence.

A1613292
LOCUS      A1613292
DEFINITION ty35g02.x1 NCI_CGAP UC-2 Homo sapiens cDNA clone IMAGE:2281106 3'
           similar to TR:Q33563 Q33563 BATRO 164 KINETOPLAST ;contains element
           MSR1 repetitive element ;, mRNA sequence.

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ACCESSION    A1613292
VERSION      A1613292.1  GI:4622459
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 28)
              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
              Emmert-Buck, M.D., Ph.D.
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html
              Trace considered overall poor quality
              Insert Length: 2324 Std Error: 0.00
              Seq primer: -40UP from Gibco
              High quality sequence stop: 1
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              Location/Qualifiers
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                  /db_xref="taxon:9606"
                  /clone="IMAGE:2281106"
                  /tissue_type="moderately-differentiated endometrial
                    adenocarcinoma, 3 pooled tumors"
                  /lab_host="DH10B"
                  /clone_lib="NCI CGAP Ut2"
                  /note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: SalI;
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                    Average insert size 1.85 kb. Life Technologies catalog #:
                    11539-012"

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 1.3e+06;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGATACCAC 11
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Db 3 AGACACCAC 13

RESULT 13
LOCUS      AZ832127
DEFINITION 2M0112M17F Mouse 10kb plasmid UGC1M library Mus musculus genomic
              clone UGC2M0112M17 F, genomic survey sequence.
              AZ832127
              AZ832127.1  GI:13002035
              GSS.
              Mus musculus (house mouse)
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)

```



Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: rdunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0354 row: F column: 10  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

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/strain="C57BL/6J"
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/clone="UUGC2M0112M17"
sex="Male"
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/clone="UUGC1M0354F10"
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Best Local Similarity 78.6%; Pred. No. 1.7e+06;  
Matches 11: Conservative 0; Mismatches 3; Indels

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||| ||| ||| |||  
1 AGAACCACAGCGCA 14

AZ510254 21 bp DNA linear GSS 05-OCT-2000  
1M0354F10R Mouse 10kb plasmid UUC1m library Mus musculus genomic  
clone UUC1m0354F10 R. genomic survey sequence.

.1 GI:10691570

Mus musculus (house mouse)  
Mus musculus  
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Nierlhausern, A. and Wright, D. Weiss, R.

TITLE	Mouse whole genome scaffolding with paired end reads from 10kbp plasmid inserts
JOURNAL	Unpublished (2000)

Query Match	61.3%	Score	9.2	DB	8	Length	21
Best Local Similarity	78.6%	Pred. No.	1.7e+06				
Matches	11	Conservative	0	Mismatches	3	Indels	

CACACGCA 14  
| | | | |  
CCCCGCA 1

AZ309912	22 bp	DNA	linear	GSS 29-SEP-2000
LOCUS				
DEFINITION				
1M0017P15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0017P15 F, genomic survey sequence.				

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

SOURCE	MUS MUSCULUS	MUS MUSCULUS (HOUSE MOUSE)
ORGANISM	Mus musculus	Mus musculus
REFERENCE	1 (bases 1 to 22)	1 (bases 1 to 22)

**AUTHORS**

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

**TITLE** Mouse whole genome  
plasmid inserts  
**JOURNAL** Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0017 row: P column: 15  
 Seq primer: CGTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 22.

FEATURES

source

1. .22  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 61.3%; Score 9.2; DB 8; Length 22;  
 Best Local Similarity 78.6%; Pred.No. 1.7e+06;  
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GATACACACGCGAG 15  
 Db 20 GGTATCATGTCAG 7

Search completed: June 23, 2005, 19:42:35  
 Job time : 2986 secs